

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 23:29:13 ; Search time 1817.54 Seconds
(without alignments)
4212.372 Million cell updates/sec

Title: US-09-380-276A-7
Perfect score: 1496
Sequence: 1 gggaaactagaaactctccaa.....aaaaaaaaaaaaaaaaaaaa 1496

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues 2236266
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_ph:*
6: gb_pl1:*
7: gb_pl2:*
8: gb_pr1:*
9: gb_pr2:*
10: gb_pr3:*
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12: gb_sy:*
13: gb_un:*
14: em_fun:*
15: em_hum1:*
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17: em_in:*
18: em_om:*
19: em_or:*
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22: em_ph:*
23: em_pl:*
24: em_ro:*
25: em_sts:*
26: em_sy:*
27: em_un:*
28: em_vl:*
29: gb_ba3:*
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32: gb_in3:*
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78: gb_sts2:*
79: gb_vil1:*
80: gb_vil2:*
81: gb_pat1:*
82: gb_pat2:*
83: em_htg0:*
84: gb_htg24:*
85: gb_pr8:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1421.4	95.0	1489	34	AF167555	AF167555 Homo sapi
2	1359.2	90.9	1364	8	AB040434	AB040434 Homo sapi
3	744.2	49.7	3964	11	AB040432	AB040432 Mus muscu
4	741	49.5	1678	11	AF167552	AF167552 Mus muscu
5	692.6	46.3	1075	11	AF173166	AF173166 Mus muscu
6	586.6	39.2	143608	73	AL161422	AL161422 Homo sapi
7	586.6	39.2	178256	72	AL139080	AL139080 Homo sapi
8	460.8	30.8	744	11	AB040433	AB040433 Mus muscu
9	460.8	30.8	886	11	AF167553	AF167553 Mus muscu
10	326.6	21.8	591	11	AF167554	AF167554 Mus muscu
c 11	73	4.9	188351	73	AL353136	AL353136 Homo sapi
c 12	73	4.9	205736	63	AC023560	AC023560 Homo sapi
13	65.4	4.4	205736	63	AC023560	AC023560 Homo sapi
14	64	4.3	3618	11	RN067080	U07080 Rattus norv
c 15	63.8	4.3	6105	12	ASPDAX3H	X85119 Artificial
c 16	63.8	4.3	6113	12	ASPDAX3C	X85118 Artificial
c 17	60.2	4.0	178273	54	AC005308	AC005308 Plasmodiu
c 18	59.6	4.0	202872	58	AC016160	AC016160 Homo sapi
19	59.2	4.0	13007	31	BM07224	U07224 Brugia mala
20	59	3.9	163443	54	AC006280	AC006280 Plasmodiu
c 21	59	3.9	196149	54	AC004709	AC004709 Plasmodiu

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c 22 58.6 3.9 318221 84 PFMAL13P3
23 58.2 3.9 899 31 AF273837
24 57.2 3.8 2260 10 AF116602
c 25 56.6 3.8 180144 63 AC023429
26 56.2 3.8 1678 53 HSHIRIP4
27 56 3.7 1775 6 AB029462
28 56 3.7 2390 10 AF090900
29 56 3.7 4435 4 XLMILZ
c 30 56 3.7 205429 54 AC005506
31 55.6 3.7 1081 4 OLA250403
32 55.6 3.7 2207 34 AK027166
33 55.4 3.7 447 34 AK026855
34 55.2 3.7 1261 7 AF243180
c 35 55 3.7 2982 32 DITSGSPA
36 54.8 3.7 470 31 AF177908
37 54.8 3.7 1582 81 A77033
38 54.8 3.7 1582 81 A77035
39 54.6 3.6 1596 32 LTRACT1596
c 40 54.6 3.6 153166 67 AC048357
41 54.6 3.6 321003 84 PFMAL4P3
42 54.4 3.6 1068 77 CNS01E0R
c 43 54.4 3.6 3138 81 A21625
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45 54.4 3.6 4615 32 DDIMANA
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ALIGNMENTS

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RESULT 1
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LOCUS Homo sapiens TAJ-alpha mRNA, complete cds.
DEFINITION AF167555
ACCESSION AF167555
VERSION AF167555.1 GI:8071643
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Eukaryota; Eutheria; Primates; Cetarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 1489)
Eby,M.F., Jamin,A., Kumar,A., Sharma,K. and Chaudhary,P.M.
TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
Activates the c-Jun N-terminal Kinase Pathway and Mediates
Caspase-Independent Cell Death
J. Biol. Chem. 275 (20), 15336-15342 (2000)
JOURNAL 10809768
PUBMED 2 (bases 1 to 1489)
REFERENCE Chaudhary,P.M.
AUTHORS Direct Submission
TITLE Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical
JOURNAL Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA
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FEATURES

source Location/Qualifiers

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361 a 366 c 380 g 382 t

BASE COUNT

ORIGIN

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Best Local Similarity 98.8%; Pred. No. 4.1e-287;
Matches 1443; Conservative 0; Mismatches 16; Indels 2; Gaps 1;

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QY 67 acaagaagaaaacgtttttcactcttttttagtattacttaggtctatttgcattgataaagtga 126
DB 87 AACAAAGAGANAACGTTTTCACCTCTTTTAGTATTACTAGGCTATTATTGTCTAATGTAAGTGA 146
QY 127 cttgtgaaacagagagactgtagacagcaagaattcaggatcggtctggaactgtgttc 186
DB 147 CTGTGAATCAGGAGACTGTAGACACACAAAGATTCAGGGATCGTCTGGAACATGTGTTC 206
QY 187 cctgcaacagtgctgggcaaggcatggagttgtctaaggaaatgctgcttcggctatgggg 246
DB 207 CCTGCAACCAAGTGTGGGCCAGGCATGGAGTTGTCTAAGGAATGTGGCTTGGGCTATGGGG 266
QY 247 aggtgcacagtgctgacgctccgctgcacaggttcaaggagagactgggcttcacaga 306
DB 267 AGATGCACAGTGTGTGGCGTCCGCTGCACAGGTTCAAGGAGGACTGGGGCTTCAGA 326
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QY 367 caaccagtgatgcatctcgtggggaactgctgacagatttttagaagaagacaaacttg 426
DB 387 CCACCAGTGTATGTCATCTGCGGGGACTGCTGTCAGGATTTTATAGGAAGACCAAACTTG 446
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DB 507 ACTGTGCCAGCAAGGTCACACTCGTGAAGATCGCGTCCACGGGCTCCAGGCCACCGGACA 566
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QY 967 ggcctctgagcagaatcccatgggtggtgacacatctctttttgtgactcttctcctg 1026
DB 987 GGCTCTGTGATGCAGATCCCATGGTGGTGGTGCACAACTCTCTTTTGTGACTCTTATCTG 1046
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Db 944 CTCCACTACCTCCAGGAGAGAACCCGGCTTCTGTGGGACACGATGCCAGCTTCT 1003
Qy 922 tcggatccctccagcagtcctctgtggtgaggttttccagctggtcctgtgatgcaga 981
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Qy 1042 acattcatctctcaatccagaaactgaaagctcaacgtcttctggattcaaatagcagtc 1101
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Qy 1102 aagatttggttgggtgggtgttccagtcagctctcatctctgaaacttttacagcagcta 1161
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Qy 1162 ctgattttatagatatataaacacacactggttagaatcagatcaactcaggtgactaa 1221
Db 1241 CACTAGACATGGTGACACTGGTACAGTCTGGGAGCAGACGCTAGCTCAGGATGCTCAA 1300
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Qy 1282 cctccagg 1290
Db 1361 CTTCCAGG 1369

RESULT 4
AF167552 1678 bp mRNA ROD 25-MAY-2000
LOCUS Mus musculus TAJ-alpha long mRNA, complete cds.
ACCESSION AF167552
VERSION AF167552.1 GI:8071637
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1678)
AUTHORS Eby, M.T., Jasmin, A., Kumar, A., Sharma, K. and Chaudhary, P.M.
TITLE TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family, Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-Independent Cell Death
J. Biol. Chem. 275 (20), 15336-15342 (2000)
10809768
JOURNAL 2 (bases 1 to 1678)
PUBMED Chaudhary, P.M.
REFERENCE Direct Submission
AUTHORS Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical
TITLE Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA
JOURNAL
FEATURES Location/Qualifiers
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Best Local Similarity 74.5%; Pred. No. 7e-145;
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Qy 142 actgtagacacaaagaattcaggatcggtctgtgaaactgtgtccctgcacacagtg 201
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Qy 262 tgacgtgcgctcacacaggttcaagagagactggggtctccagaaatgcagacccctgc 321
Db 289 TGCCCTGAGGCCCGCACCGGTTCAAGGAAGACTTGGGGTTTCAGAAAGTGTAAAGCCATGTG 348
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QY 1282 cctccagg 1290
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Db 1306 CTTCCAGG 1314

RESULT 5
AF173166 AF173166 1075 bp mRNA ROD 26-DEC-1999
LOCUS Mus musculus TNFRSF19 mRNA, complete cds.
DEFINITION AF173166
ACCESSION AF173166
VERSION AF173166.1 GI:6635354
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1075)
AUTHORS Hu, S., Tamada, K., Ni, J., Vincenz, C. and Chen, L.
TITLE Characterization of TNFRSF19, a novel member of the tumor necrosis
factor receptor superfamily
JOURNAL Genomics 62 (1), 103-107 (1999)
MEDLINE 20054362
REFERENCE 2 (bases 1 to 1075)
AUTHORS Hu, S.
TITLE Direct Submission
JOURNAL Submitted (29-JUL-1999) Department of Immunology, Mayo Clinic and
Foundation, 200 First Street SW, Rochester, MN 55905, USA
FEATURES
source 1..1075
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CDS 28..1074
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TVSSPRDTALAIVICSAATVLLALLILCVIKRQFMKPKPSWLSRPQDIQVNGSEL
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SLNPEMLCFRFDL"
BASE COUNT 211 a 308 c 296 g 259 t 1 others
ORIGIN

Query Match 46.3%; Score 692.6; DB 11; Length 1075;
Best Local Similarity 78.7%; Pred. No. 8.9e-135;
Matches 840; Conservative 0; Mismatches 224; Indels 3; Gaps 1;

QY 22 aataaatacatattgataagaagatggcttttaaaagtgtactactagaacaagagaaaaactg 81
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RESULT 6

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LOCUS      Homo sapiens chromosome 13 clone RP11-168G12, *** SEQUENCING IN
DEFINITION      PROGRESS ***, 3 unordered pieces.
ACCESSION      AL161422
VERSION      AL161422.13 GI:10277928
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
              1 (bases 1 to 143608)
REFERENCE      Pearce,A.
AUTHORS      Direct Submission
TITLE      Submitted (19-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,
JOURNAL      CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
              requests: clonerequest@sanger.ac.uk
              On Sep 22, 2000 this sequence version replaced gi:10190601.
COMMENT      ----- Genome Center
              Center: Sanger Centre
              Center code: SC
              Web site: http://www.sanger.ac.uk
              Contact: humquery@sanger.ac.uk
              ----- Project Information
              Center project name: BA168G12
              ----- Summary Statistics
              Assembly program: XGAP4; version 4.5
              Sequencing vector: plasmid; L08752; 100% of reads
              Chemistry: Dye-terminator Big Dye; 100% of reads
              Consensus quality: 143007 bases at least Q40
              Consensus quality: 143260 bases at least Q30
              Consensus quality: 143347 bases at least Q20
              Insert size: 143408; sum-of-contigs
              Insert size: 145175; 5.9% error; agarose-fp
              Quality coverage: 8.55x in Q20 bases; sum-of-contigs Quality
              coverage: 8.58x in Q20 bases; agarose-fp
              -----
              * NOTE: This is a 'working draft' sequence. It currently
              * consists of 3 contigs. The true order of the pieces
              * is not known and their order in this sequence record is
              * arbitrary. Gaps between the contigs are represented as
              * runs of N, but the exact sizes of the gaps are unknown.
              * This record will be updated with the finished sequence
              * as soon as it is available and the accession number will
              * be preserved.
              *
              * 1 2992: contig of 2992 bp in length
              *
              * 2993 3092: gap of 100 bp
              *
              * 3093 129375: contig of 126283 bp in length
              *
              * 129376 129475: gap of 100 bp
              *
              * 129476 143608: contig of 14133 bp in length.
              *
              FEATURES
              source      Location/Qualifiers
              1..143608
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /chromosome="13"
              /clone="RP11-168G12"
              /clone_lib="RPCI-11.1"
              1..2992
              /note="assembly_fragment:01799
              fragment_chain:1"
              3093..129375
              /note="assembly_fragment:02957
              fragment_chain:1
              clone_end:T7
              vector_side:left"
              129476..143608
              /note="assembly_fragment:00106"
              BASE COUNT      41121 a 29506 c 30419 g 42362 t 200 others
              ORIGIN

Query Match      39.28; Score 586.6; DB 73; Length 143608;
Best Local Similarity      97.7%; Pred. No. 1.8e-112;

```

```

Matches 595; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy 882 agaaacagccagccagccgggagagatggtccgactttcttcgataccctcacagctcc 941
Db 84813 AGAAACGACGCGCCAGCGGGAGATGGTCCGACTTTCTTCGGATCCCTCACCAGTCC 84872
Qy 942 atctgtgagagttttcagatgcctgctgctgagatcccatggtggtggtgacac 1001
Db 84873 ATCTGTGGCGAGTTTTCAGATGCCTGGCCTCTGATGAGATCCATGGGTGGTGAAC 84932
Qy 1002 atctcttttctgactcttctcctgaactcactggaagacatctctctcctcaatcca 1061
Db 84933 ATCTCTTTTGTGACTCTTATCTCTGAATCACTACTGGAGAAGACATTCATCTCTCAATCCA 84992
Qy 1062 gaacttaaaagctcaacgctcttctgattcaaatagcagctcaagatttgggtggggtc 1121
Db 84993 GAACCTTAAAGCTCAACGCTCTTTGGATTCAANTAGCAGTCAAGATTGGTTGGTGGGCT 85052
Qy 1122 gtccagtcagctcattctgaaactttacagcagctactgtattctctagataaac 1181
Db 85053 GTTCCAGTCCAGTCTCATCTCTGAAACTTTACAGCAGCTACTGATTTATCTAGATATAAC 85112
Qy 1182 aacacactggtagatcagcatcaactcagcagctacactaatactatgagaagccagctagat 1241
Db 85113 AACACACTGGTAGAATCAGCATCAACTCACTCAGATGCACCTAATATGAGAAGCCAGCTAGAT 85172
Qy 1242 cagagagtgctgctatccatcccccagccactcagacgctccctccaggttaagcagcga 1301
Db 85173 CAGGAGAGTGTGCTGTCTATCCACCAGCCACTCAGAGCTCCCTCCAGGTAAAGCAGCGA 85232
Qy 1302 ctggttccctctgtgaacacagcactgactacagtagatcagaactctgttcccgagcata 1361
Db 85233 CTGGGTTCCCTGTGAACACACAGCAGCTGACTTACAGTAGATCAGAGCTCTGTTCCCGAGCATA 85292
Qy 1362 agattgggggaacctgagtgatttttttttgatctcttctaattctctgtatgtt 1421
Db 85293 AGATTGGGGGAACCTGATGAGTTTTTTTTTGTGATCTTTTAATAATTTCTTTGTGTTGT 85352
Qy 1422 agagtatgttttaaaataaattcaagtatttttttaaaactaaaaaataaaaaaa 1481
Db 85353 AGAGTAGTGTTTTAAATATAATTTCAAGTATTTTTTAAATAAATAACACACTAATATAT 85412
Qy 1482 aaaaaaaa 1490
Db 85413 AAGAGCAA 85421

RESULT      7
AL139080      178256 bp      DNA      HTG      29-SEP-2000
LOCUS      Homo sapiens chromosome 13 clone RP11-173N17 map q12.11-12.3, ***
DEFINITION      SEQUENCING IN PROGRESS ***, 15 unordered pieces.
ACCESSION      AL139080
VERSION      AL139080.8 GI:10443032
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
              1 (bases 1 to 178256)
REFERENCE      Burton,J.
AUTHORS      Direct Submission
TITLE      Submitted (28-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,
JOURNAL      CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
              requests: clonerequest@sanger.ac.uk
              On Oct 1, 2000 this sequence version replaced gi:10129398.
COMMENT      ----- Genome Center
              Center: Sanger Centre
              Center code: SC
              Web site: http://www.sanger.ac.uk
              Contact: humquery@sanger.ac.uk
              ----- Project Information
              Center project name: BA173N17

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```

----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid: L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 168976 bases at least Q40
Consensus quality: 172107 bases at least Q30
Consensus quality: 173780 bases at least Q20
Insert size: 176856; sum-of-contigs
Insert size: 163577; 8.6% error; agarose-fp
Quality coverage: 3.73x in Q20 bases; sum-of-contigs Quality
coverage: 4.07x in Q20 bases; agarose-fp

```



```
|||||
Db 47171 AGAGTATCTTTTAAATAAATTTCAAGTATTTTAAAAAACTTAACACAGCTAATATAT 47230
Qy 1482 aaaaaaaa 1490
Db 47231 AAGAGCAAA 47239

RESULT 8
AB040433 744 bp mRNA ROD 22-JUL-2000
LOCUS Mus musculus mRNA for dTROY, complete cds.
DEFINITION AB040433
ACCESSION AB040433
VERSION AB040433.1 GI:9392327
KEYWORDS dTROY.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (sites)
AUTHORS Kojima,T., Morikawa,Y., Copeland,N.G., Gilbert,D.J., Jenkins,N.A.,
Senba,E. and Kitamura,T.
TITLE TROY, a newly identified member of the tumor necrosis factor
receptor superfamily, exhibits a homology with Edar and is
expressed in embryonic skin and hair follicles
J. Biol. Chem. 275 (27), 20742-20747 (2000)
20347167
2 (bases 1 to 744)
AUTHORS Kojima,T. and Kitamura,T.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2000) to the DDBJ/EMBL/GenBank databases. Tetsuo
Kojima, Chugai Research Institute for Molecular Medicine, Inc.,
Cytokine Research Program; 153-2 Nagai, Niihari, Ibaraki 300-4101,
Japan (E-mail:kojimat@ciimmed.com, Tel:81-298-306211,
Fax:81-298-306270)
FEATURES
source Location/Qualifiers
1. 744
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="14"
67. 711
/gene="dTroy"
67. 711
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/notes="a member of TNFR superfamily exhibits a homology
with Edar"
/codon_start=1
/product="dTROY"
/protein_id="BAB03268.1"
/db_xref="GI:9392328"
/translation="MALKVLPPLHRTVLFALFLHLACKVSCETGDCRQOEKDRSG
NCVLCKGPGMELSKECGEGYGEDAOCVCPHRFKEDWGFQKCKPCADCALVNRQ
RVCSHTSDAVCGDCLPGFRKYLGVQDMECVPCGDPDPPEPHCTSKVNLVKISS
TVSSPRDTALAAVICSALATVLLALLILCVYCKRQPMERKPKSLCLTVK"
BASE COUNT 162 a 208 c 211 g 163 t
ORIGIN
Query Match 30.8%; Score 460.8; DB 11; Length 744;
Best Local Similarity 81.9%; Pred. No. 2.5e-86;
Matches 531; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
Qy 22 aataaatacattgataagaagatgctttaaaagtctactagaacaagagaaaacgt 81
Db 44 AATAACACGTTTGTGTAGAGCCATGGCAGCTCAAGTCTTACCTTACACAGGACGGTGC 103
Qy 82 ttttcactcttttagtattagctattgttcattgataaagtgaactgtgtgaacaggag 141
Db 104 TCTTCGCTGCCATTCTCTCTCTCCACCTTGGCATGTGAAAGTGAGTGGCGAAACCGGAG 163
Qy 142 actgtagacagcaagaatctcaggatcggctgtggaactgtgttccctgcacacagtg 201
Db 164 ATTGCAGGCAGGAGTAATCAAGGATCGATCTGGAAGTGTGTCTCTCTGCAAAACAGTGG 223
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Qy 202 ggcaggcatgagttgttctaagaataatgcttgcgtatggggagagatcacacagtgtg 261
Db 224 GACCTGGCATGAGTTGTCCCAAGGAATGTGCTTCGGGTATGGGAGGATGCACAGTGTG 283
Qy 262 tgacgtgccggtgcacaggttcaaggaggactggggttccagaaaatgcgaagccctgtc 321
Db 284 TGCCCTGCAGGCCGACCCGGTTCAAGGAAGACTGGGGTTTCCAGAAAGTTAAGCCATGTG 343
Qy 322 tggactgcagtgagtggaaccgcttccagaaggcaaatgttccagccaccagtgatgcca 381
Db 344 CGGACTGTGCGCTGTGTGAACCGCTTTCAGAGGGGCCAACTGTCTACACACACAGTGTG 403
Qy 382 tctcggggactgcttgcagattttatagaagacaaaacttgcgcttccaagaca 441
Db 404 TCTCGGGGACTGCTGTCAGGATTTTACCGGAAGACCAAACTGGTGTGTTTCAAGACA 463
Qy 442 tggagtgtgcttgtgagaccctctctctcttcttccagaaacccgctgtgcagcaagg 501
Db 464 TGGAGTGTGCTCTGCGAGACCCACCTCTCTCCCTACGAAACACACTGTACCAGCAAGG 523
Qy 502 tcaactcgtgaagatcgcgtccacggctccagccacgggacacggcgtggctgcgcg 561
Db 524 TGAACCTTGTGAAGATCTCTCCACCGCTCTCCAGCCCTCGGACACACGGCGTGGTGGCG 583
Qy 562 ttatctgcagcgtctgcaccgctcctgcgtggccctcctcctcctcctcctcctcctt 621
Db 584 TCATCTGACGTGCTCTGCCACGGTGTGCTGCGCTCTCTCTCTCTCTCTCTCTCTACT 643
Qy 622 gtaagacagatttatgagaagaacccagctggctgtcctgcgggtcac 669
Db 644 GCAAGAGCGAGTTCATGTGAGAAGAAACCCAGCTGTGAAGCTCCCATCCC 691

RESULT 9
AF167553 886 bp mRNA ROD 25-MAY-2000
LOCUS Mus musculus TAJ-alpha short mRNA, complete cds.
DEFINITION AF167553
ACCESSION AF167553
VERSION AF167553.1 GI:8071639
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 886)
AUTHORS Eby,M.T., Jasmin,A., Kumar,A., Sharma,K. and Chaudhary,P.M.
TITLE TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
Activates the c-Jun N-terminal Kinase Pathway and Mediates
Caspase-Independent Cell Death
J. Biol. Chem. 275 (20), 15336-15342 (2000)
10809768
PUBMED 2 (bases 1 to 886)
AUTHORS Chaudhary,P.M.
TITLE Direct Submission
JOURNAL Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical
Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA
FEATURES
source Location/Qualifiers
1. 886
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="Soares p3NMF19.5"
72. 716
/notes="decoy receptor"
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NCVLCKGPGMELSKECGEGYGEDAOCVCPHRFKEDWGFQKCKPCADCALVNRQ
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BASE COUNT 204 a 245 c 247 g 190 t
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1368..2402
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2503..3524
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17069..20185
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20286..22634
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22735..27012
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27113..29342
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vector_side:right
29443..33381
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36663..40982
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45621..50823
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50724..55610
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73580..80554
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89414..98132
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Query Match
Best Local Similarity 4.9%; Score 73; DB 63; Length 205736;
Matches 121; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

Qy 223 aggaatgtgcttcggtatgggagagatgcacagtgtgtgacgtgccggtgcacaggt 282
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 79395 AGATTGTGTTATGAGAGAGGTGGAGATGCTACTGCACAGCTGCCCTCTCGCAGT 79336

Qy 283 tcaagagagatgggcttcgaagaaatgaagccctgtctgactgcgcagtggtgaacc 342
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 79335 ACAAAGACAGCTGGGGCCACCACAGATGTCAGAGTTGCATCACCTGTGTCATCAATC 79276

Qy 343 gctttcagaagcaaatgttcagccaccagtcagtcagtcagtcagtcagtcagtcag 402
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 79275 GTGTCAGAGAGTCAACTGCACAGCTACCTCTAATGCTGTCTGTGGGACTGTTGCCCA 79216

Qy 403 gattttataggaagacgaac 423
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DB 79215 GGTGAGCTGCTTTATGAGAC 79195

RESULT 13

AC023560 205736 bp DNA HTG 12-MAR-2000

LOCUS AC023560

DEFINITION Homo sapiens chromosome 17 clone RP11-85I20 map 17, WORKING DRAFT

SEQUENCE, 34 unordered pieces.

AC023560

VERSION AC023560.2 GI:7229913

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 205736)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 17, clone RP11-85I20

Unpublished

2 (bases 1 to 205736)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Largocque, K., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrum, J., Meneus, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Olivari, T. M., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission

Submitted (15-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Mar 12, 2000 this sequence version replaced gi:6978256.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIER

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L6741

Center clone name: 85_L20

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 178566 bases at least Q40

Consensus quality: 190940 bases at least Q30

Consensus quality: 197088 bases at least Q20

Insert size: 194000; agarose-fp

Insert size: 202436; sum-of-contigs

Quality coverage: 4.2 in Q20 bases; agarose-fp

Quality coverage: 4.0 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as

```

* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

1267:	contig of 1267 bp in length
1367:	gap of 100 bp
1368:	2402: contig of 1035 bp in length
2503:	3524: contig of 100 bp
3525:	3624: gap of 100 bp
3625:	4913: contig of 1289 bp in length
4914:	5013: gap of 100 bp
5019:	6289: contig of 1276 bp in length
6290:	6389: gap of 100 bp
6390:	7655: contig of 1266 bp in length
7656:	gap of 100 bp
7756:	9267: contig of 1512 bp in length
9367:	gap of 100 bp
9368:	11138: contig of 1771 bp in length
11239:	11238: gap of 100 bp
11239:	13822: contig of 2584 bp in length
13823:	13922: gap of 100 bp
13923:	16968: contig of 3046 bp in length
16969:	17068: gap of 100 bp
17069:	20185: contig of 3117 bp in length
20186:	20285: gap of 100 bp
20286:	22634: contig of 2349 bp in length
22635:	22734: gap of 100 bp
22735:	27012: contig of 4278 bp in length
27013:	27112: gap of 100 bp
27113:	29342: contig of 2230 bp in length
29343:	29442: gap of 100 bp
29443:	33361: contig of 3939 bp in length
33382:	33481: gap of 100 bp
33482:	36562: contig of 3081 bp in length
36563:	36662: gap of 100 bp
36663:	40982: contig of 4320 bp in length
40983:	41082: gap of 100 bp
41083:	45520: contig of 4438 bp in length
45521:	45620: gap of 100 bp
45621:	50623: contig of 5003 bp in length
50624:	50723: gap of 100 bp
50724:	55610: contig of 4887 bp in length
55611:	55710: gap of 100 bp
55711:	61038: contig of 5328 bp in length
61039:	61138: gap of 100 bp
61139:	66159: contig of 5021 bp in length
66160:	66259: gap of 100 bp
66260:	73479: contig of 7220 bp in length
73480:	73579: gap of 100 bp
73580:	80554: contig of 6975 bp in length
80555:	80654: gap of 100 bp
80655:	89313: contig of 8659 bp in length
89314:	89413: gap of 100 bp
89414:	98132: contig of 8719 bp in length
98133:	98232: gap of 100 bp
98233:	107469: contig of 9237 bp in length
107470:	107569: gap of 100 bp
107570:	117873: contig of 10304 bp in length
117874:	117973: gap of 100 bp
117974:	130973: contig of 13000 bp in length
130974:	131073: gap of 100 bp
131074:	143236: contig of 12163 bp in length
143237:	143336: gap of 100 bp
143337:	154478: contig of 11142 bp in length
154479:	154578: gap of 100 bp
154579:	169967: contig of 15389 bp in length
169968:	170067: gap of 100 bp
170068:	187347: contig of 17280 bp in length
187348:	187447: gap of 100 bp
187448:	205736: contig of 18289 bp in length.

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/organism="Homo sapiens"
/obj_xref="taxon:9606"
/chromosome="17"
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Query Match 4.48; Score 65.4; DB 63; Length 205736;

Best Local Similarity 38.6%; Pred. No. 0.0016;

Best local similarity 38.0%, FREQ NO: 0.0010,
Matches 114; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

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[illegible]

Ov 283 tcaaggaggactggggacttccagaaatgcaagccctgtctggactcgcgactggtgaacc 342

QY 283 LCACAGGAGGACGCGGGGCLCCACAGAAACGACGCCCCGCTGCGACGCGCGCGAGCGGCGAACCC 34

Db 154361 ACACAAGCAGCTGGGSCCACCACACATGTGACAGAGATGSCATCACCTGTGCTGTGTCATCAATC 154

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 23:32:11 : Search time 88.06 seconds
(without alignments)
6381.914 Million cell updates/sec

Title: US-09-380-276A-7
Perfect score: 1496
Sequence: 1 gggaacgtagaactctccaa.....aaaaaaaaaaaaaaaaaaaaa 1496

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 18781343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_36:*

1: /cgn2_2/gcgdata/geneseq/geneseq/NA1980.DAT:*

2: /cgn2_2/gcgdata/geneseq/geneseq/NA1981.DAT:*

3: /cgn2_2/gcgdata/geneseq/geneseq/NA1982.DAT:*

4: /cgn2_2/gcgdata/geneseq/geneseq/NA1983.DAT:*

5: /cgn2_2/gcgdata/geneseq/geneseq/NA1984.DAT:*

6: /cgn2_2/gcgdata/geneseq/geneseq/NA1985.DAT:*

7: /cgn2_2/gcgdata/geneseq/geneseq/NA1986.DAT:*

8: /cgn2_2/gcgdata/geneseq/geneseq/NA1987.DAT:*

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12: /cgn2_2/gcgdata/geneseq/geneseq/NA1991.DAT:*

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14: /cgn2_2/gcgdata/geneseq/geneseq/NA1993.DAT:*

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16: /cgn2_2/gcgdata/geneseq/geneseq/NA1995.DAT:*

17: /cgn2_2/gcgdata/geneseq/geneseq/NA1996.DAT:*

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19: /cgn2_2/gcgdata/geneseq/geneseq/NA1998.DAT:*

20: /cgn2_2/gcgdata/geneseq/geneseq/NA1999.DAT:*

21: /cgn2_2/gcgdata/geneseq/geneseq/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1496	100.0	1496	19 V33362	Nucleotide sequenc
2	1494.4	99.9	1502	20 X08689	Novel nucleotide s
3	1421.4	95.0	1489	20 X23415	Human hAPO4-alpha
4	1288.8	85.1	1704	19 V33361	Nucleotide sequenc
5	1276.4	85.3	2185	20 X24978	Human TRAIN-R CDNA
6	835.6	55.9	987	20 X59346	Human NTR-5 CDNA
7	741	49.5	1678	20 X23413	Mouse hAPO4-alpha
8	460.8	30.8	886	20 X23414	Mouse hAPO4-alpha
9	460.8	30.8	942	20 X24977	Mouse TRAIN-R (lon
10	460.8	30.8	981	20 X87394	Mouse STRIFE1 (Tan
11	447.2	29.9	893	20 X84622	Human TNFR superfa
12	362.6	24.2	538	20 X59345	Mouse NTR-5 CDNA

13	361.6	24.2	371	19 V11422	Human secreted pro
14	326.6	21.8	591	20 X23417	Mouse hAPO4-gamma
15	326.6	21.8	599	20 X24976	Mouse TRAIN-R (sho
16	326.6	21.8	623	20 X84623	Mouse TNFR superfa
17	326.6	21.8	636	21 X29208	CDNA encoding murI
18	326.6	21.8	655	20 X87395	Mouse STRIFE2 (Tan
19	154.8	10.3	932	21 X29411	CDNA encoding huma
20	121.8	8.1	1133	20 X23416	Rat hAPO4-alpha DN
21	90.4	6.0	791	20 X24979	Clone GJ156 encodi
22	87.4	5.8	181	19 V11423	Human secreted pro
23	87.4	5.8	201	20 X86655	EST clone AX92. H
24	82	5.5	396	20 X23418	Mouse hAPO4-beta D
25	81.2	5.4	546	21 X29410	CDNA encoding huma
26	77.8	5.2	474	21 X29209	CDNA encoding huma
27	57	3.9	1584	21 D00015	Scorpion protein d
28	57	3.8	1443	21 A26291	Human secreted pro
29	56.8	3.8	1883	19 V59670	Human secreted pro
30	54.8	3.7	1558	17 T28255	Survival motor neu
31	54.8	3.7	1560	17 T18828	Human survival mot
32	54.8	3.7	1582	17 T28259	Survival motor neu
33	54.8	3.7	1582	17 T18831	Human survival mot
34	54.4	3.6	2271	20 V84632	Human secreted pro
35	54.4	3.6	2276	20 V84583	Human secreted pro
36	54.4	3.6	3138	12 Q11712	Shuttle vector pMU
37	54.2	3.6	1969	20 X60804	Human secreted pro
38	53.6	3.6	3809	21 A23440	CDNA encoding huma
39	53	3.5	2007	19 V40754	C. felis esterase,
40	53	3.5	2007	19 V40755	C. felis esterase,
41	52.8	3.5	664	21 A26336	Human secreted pro
42	52.8	3.5	2933	21 X293703	PRO172 DNA35916-11
43	52.8	3.5	5173	18 T89783	Human Immunodefici
44	52.6	3.5	1420	18 T72167	Alzheimer's diseas
45	52.6	3.5	3238	16 Q83532	Sequence encoding

ALIGNMENTS

RESULT 1

V33362

ID V33362 standard; CDNA to mRNA; 1496 BP.

XX

AC V33362;

DT 02-DEC-1998 (first entry)

DE Nucleotide sequence of human beta-OAF065.

XX Human; beta-OAF065; stroma cell; antibody; inflammatory;

KW cytokine-mediated disease; rheumatism; ulcerative colitis; ss.

XX Homo sapiens.

OS

FH Key Location/Qualifiers

FT CDS 45..1316

FT /*tag= a

FT /*product= "human beta-OAF065 protein"

FT /*tag= b

FT /*tag= c

FT mat_peptide 120..1313

FT /*tag= c

FT /*transl_except= (pos:711..713, aa= pro)

FT /*transl_except= (pos:714..716, aa= Arg)

XX WO9838304-A1.

PD 03-SEP-1998.

XX 26-FEB-1998; 98WO-JP00799.

XX 27-FEB-1997; 97JP-0043143.

XX (ONOY) ONO PHARM CO LTD.

XX PI Fukushima D, Konishi M, Tada H;
 XX DR WPI: 1998-481205/41.
 XX DR P-PSDB: W70387.
 XX PT Membrane polypeptide expressed by human stroma cells, and antibodies
 XX PT recognising it - for treatment of inflammatory and other
 XX PT cytokine-mediated diseases.
 XX PS Disclosure; Pages 40-41; 54pp; Japanese.
 XX CC This is the nucleotide sequence of the human beta-OAF065, used in
 CC the method of the invention. The process involves the use of peptides
 CC expressed by stroma cells, and its antibodies are used for in the
 CC prevention and treatment of inflammatory and other cytokine-mediated
 CC diseases such as rheumatism, ulcerative colitis.
 XX CC
 XX SQ Sequence 1496 BP; 388 A; 360 C; 372 G; 376 T; 0 other;

Query Match 100.0%; Score 1496; DB 19; Length 1496;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1496; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gggaaacgtagaactctccaacaataaatacatattgataagaagatggctttaaaagtgc 60
 DB 1 gggaaacgtagaactctccaacaataaatacatattgataagaagatggctttaaaagtgc 60

QY 61 tactagaaacagaaacacgtttttcactcttttagtattactaggctatttgcattgta 120
 DB 61 tactagaaacagaaacacgtttttcactcttttagtattactaggctatttgcattgta 120

QY 121 aagtgacttgtaaacaggagactgtagacagaagaataatcagggatcggctcggaaact 180
 DB 121 aagtgacttgtaaacaggagactgtagacagaagaataatcagggatcggctcggaaact 180

QY 181 gtgttcctccaaacacagtgctggccagggcatggagtgcttaaggaaatgtggttcggct 240
 DB 181 gtgttcctccaaacacagtgctggccagggcatggagtgcttaaggaaatgtggttcggct 240

QY 241 atggggaggatgcacagtgctgtgacgtgcgggctgcacaggttcaaggaggaactggggct 300
 DB 241 atggggaggatgcacagtgctgtgacgtgcgggctgcacaggttcaaggaggaactggggct 300

QY 301 tccagaatcaagccctgctggactgcgcagtggtgaaaccgctttcagaaggaact 360
 DB 301 tccagaatcaagccctgctggactgcgcagtggtgaaaccgctttcagaaggaact 360

QY 361 gttcagccacagtgatgccatctgcgggactgctgtgccagatattataggaaagcga 420
 DB 361 gttcagccacagtgatgccatctgcgggactgctgtgccagatattataggaaagcga 420

QY 421 aactgtgcggtttcaagacatggagtggtgacctgtggagaccctcctcctctacg 480
 DB 421 aactgtgcggtttcaagacatggagtggtgacctgtggagaccctcctcctctacg 480

QY 481 aaccgcaactgtccagcaaggatcaacctctgaagatcgcggtccacggctccagccac 540
 DB 481 aaccgcaactgtccagcaaggatcaacctctgaagatcgcggtccacggctccagccac 540

QY 541 gggacagcggcgtggctgcccgttatctgcagcgcctctggccacctgctggtccctgc 600
 DB 541 gggacagcggcgtggctgcccgttatctgcagcgcctctggccacctgctggtccctgc 600

QY 601 tcactcctgtgtoactctattgtaagagacagtttatggagaagaacacccagctggctc 660
 DB 601 tcactcctgtgtoactctattgtaagagacagtttatggagaagaacacccagctggctc 660

QY 661 tgcggtcacaggacattcattacaacggctctgagctgctgctgtcttgacagacctcagc 720
 DB 661 tgcggtcacaggacattcattacaacggctctgagctgctgctgtcttgacagacctcagc 720

QY 721 tccacgaatatgccacagagcctgctgccagtgcgcgcctgactcagtgacagacctgcg 780
 DB 721 tccacgaatatgccacagagcctgctgccagtgcgcgcctgactcagtgacagacctgcg 780

QY 781 ggcgggtgcgcttgctcccatccatgtgctgtgagaggcctgcagcccaacccggcga 840
 DB 781 ggcgggtgcgcttgctcccatccatgtgctgtgagaggcctgcagcccaacccggcga 840

QY 841 ctcttggtgtgggtgctattctgcagcagcttcttcaggcaagaacagcaggccagccg 900
 DB 841 ctcttggtgtgggtgctattctgcagcagcttcttcaggcaagaacagcaggccagccg 900

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 DB 1021 atcctgaactcactgggagaagacattcattctctcaatccagaaacttgaaagctcaact 1080

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QY 1141 ctgaaaaactttacagcagctactgatttatctagatataacaacacactggttagaatcag 1200
 DB 1141 ctgaaaaactttacagcagctactgatttatctagatataacaacacactggttagaatcag 1200

QY 1201 catcaactcaggatgcactaactatgagaagccagctagatcaggagagtggcgctatca 1260
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QY 1261 tccaccagccactcagacgtccctccaggtgaaggcagcagctgggttccctgtggaacac 1320
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 DB 1381 gacttttttttgcacttttaataattctctgtatgttagagatgttttaaaataa 1440

QY 1441 atttcaagtatttttttaaaactaaaaaataaaaaaataaaaaaataaaaaa 1496
 DB 1441 atttcaagtatttttttaaaactaaaaaataaaaaaataaaaaaataaaaaa 1496

RESULT 2
 X08689
 ID X08689 standard; cDNA; 1502 BP.
 XX AC X08689;
 XX DT 27-SEP-1999 (first entry)
 XX DE Novel nucleotide sequence encoding new protein (Clone AX92_3).
 XX KW Polynucleotide; protein; nutrition; cytokine; cell proliferation;
 KW cell differentiation; immunostimulation; immunosuppression;
 KW haematopoiesis regulation; tissue growth; activin; inhibin;
 KW chemotaxis; chemokinesis; haemostasis; thrombolysis; receptor;
 KW ligand; anti-inflammatory; tumour suppression; gene therapy; ds.
 XX OS Homo sapiens.
 XX FT Key
 CDS Location/Qualifiers
 51..1322

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FT      /*tag= a
FX      /product= "Novel protein"
FX      WO9920644-A1.
PN      29-APR-1999.
XX      16-OCT-1998; 98WO-US22034.
PD      18-OCT-1997; 97US-0955557.
XX      (GEMY ) GENETICS INST INC.
XX      Agostino MJ, Bowman MR, Evans C, Jacobs K, Lavallie ER;
PI      McCoy JM, Merberg D, Racie LA, Spaulding V, Treacy M;
XX      WPI: 1999-288272/24.
DR      P-PSDB; W85724.
XX      New polynucleotides encoding secreted human proteins
XX      Claim 32; Page 116; 136pp; English.
XX      The new human secreted proteins are encoded by polynucleotides
CC      obtained from human placenta, adult testes, fetal kidney, fetal
CC      brain, adult brain, adult brain and adult blood cDNA libraries.
CC      The polynucleotides and proteins are predicted to have biological
CC      activities which would make them suitable for treating, preventing or
CC      ameliorating medical conditions in humans and animals. Suggested
CC      activities include nutritional activity, cytokine and cell
CC      proliferation/differentiation activity, immune stimulating (e.g. as
CC      vaccines) or suppressing activity, haematopoiesis regulating
CC      activity, tissue growth activity, activin/inhibin activity,
CC      chemotactic/chemokinetic activity, haemostatic and thrombolytic
CC      activity, receptor/ligand activity, anti-inflammatory activity,
CC      adherin/tumour invasion suppressor activity, and tumour inhibition
CC      activity. The polynucleotides are also stated to be useful for gene
CC      therapy. The sequences are identified by a secretory leader
CC      sequence motif in the polynucleotide and it is thought that the
CC      encoded proteins have biological activity by virtue of their secreted
CC      nature. This clone was designated AX92_3. A probe for this clone is
CC      described in X08704.
XX      Sequence 1502 BP; 388 A; 362 C; 375 G; 377 T; 0 other;
SQ      Query Match      99.9%; Score 1494.4; DB 20; Length 1502;
      Best Local Similarity 99.9%; Pred. No. 0;
      Matches 1495; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      61 tactagaacaagaaaacgtttttcactcttttagtattactagggtatttgcattga 120
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Qy      121 aagtgaacttgaaacaggaactgtagacagcaagaattcagggaactcggtcgaaact 180
Db      127 aagtgaacttgaaacaggaactgtagacagcaagaattcagggaactcggtcgaaact 186
Qy      181 gtgtccctcgaaccagtggtggcagcagtgagttgtctaaagaaatgtggttcgact 240
Db      187 gtgtccctcgaaccagtggtggcagcagtgagttgtctaaagaaatgtggttcgact 246
Qy      241 atgggagagatgcacagtgtgtgacgtgccggtgcacaggttcaagagagactgggct 300
Db      247 atgggagagatgcacagtgtgtgacgtgccggtgcacaggttcaagagagactgggct 306
Qy      301 tccagaaatgcaagccctgtctggaactgcgcaagtgtgaaacgccttccagaagcgaatt 360
Db      307 tccagaaatgcaagccctgtctggaactgcgcaagtgtgaaacgccttccagaagcgaatt 366
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Qy      361 gttcagccaccagtgatgccatctgcggggactgcttgccaggatttttataggagacga 420
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Qy      421 aacttgctggctttcaagacatggagtgctgcttggagacctctctctctacg 480
Db      427 aacttgctggctttcaagacatggagtgctgcttggagacctctctctctacg 486
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Db      487 aaccgcaactgtgccagcaaggctcaacctctgtaagatcgctccacggcctccagccac 546
Qy      541 gggacagggcgtgctgcttctatctgcagcgtctctgaccacgtctctggtccctgc 600
Db      547 gggacagggcgtgctgcttctatctgcagcgtctctgaccacgtctctggtccctgc 606
Qy      601 tcatctctgtgtcatctatttgaagacagatttatgagaagaacccagctggtctc 660
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Qy      781 ggcggctgcgcttgctcccatccatgtgctgagggagcctgcagcccaacccggcga 840
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Db      1147 ctgaaaactttacagcagctactgatttatctagatataacaacacactggtagaactcag 1206
Qy      1201 catcaactcaggatgacactaactatgagaacccagctagatcaggagagtggtcgctatca 1260
Db      1207 catcaactcaggatgacactaactatgagaacccagctagatcaggagagtggtcgctatca 1266
Qy      1261 tccacccagcactcagacgtccctccaggttaagcagcagctgggttccctgtgaaacac 1320
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Qy      1321 agcactgacttacagtagatcagaactctgttcccagcataagatttggggaaactgat 1380
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Db 681 cggcgctggcgttctatctgcagcgtctgcccacgctcgtggtccctgctcatcc 740
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Db 741 tctgtgcatctattgtaagagacagtttatggagaagaacccagctggtctctcggt 800
Qy 667 cacaggacattcagtacacagcgtctgagctgctgctgcttcttgacagacctcagctcacg 726
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Qy 1267 cagccactcagacgtccctccaggta 1292
Db 1401 cagccactcagacgtccctccaggtaa 1426

RESULT 6
X59346
ID X59346 standard; cDNA; 987 BP.
AC XX
AC X59346;
DT 20-SEP-1999 (first entry)
XX XX
DE Human NTR-5 cDNA.
KW NTR-5; human; receptor; signal transduction; bone; muscle;
KW diagnosis; therapy; ss.
OS Homo sapiens.
XX XX
FH Key Location/Qualifiers
FT sig_peptide 1..57
FT /*tag= a
FT mat_peptide 58..987
FT /*tag= b
XX XX

PN WO9933967-A2.
XX XX
PD 08-JUL-1999.
XX XX
PF 28-DEC-1998; 98WO-US27688.
XX XX
PR 29-DEC-1997; 97US-0068925.
XX XX
PA (REGG-) REGENERON PHARM INC.
XX XX
PI Valenzuela DM;
XX XX
DR WPI; 1999-419102/35.
DR P-PSDB; Y06400.
XX XX
PT New mammalian receptor NTR-5 polypeptides
XX XX
PS Claim 2a; Page 21-22; 27pp; English.
XX XX
CC This is the claimed coding region of human cDNA encoding a novel
CC receptor, designated NTR-5 (see Y06400), that shows homology to
CC osteoprotegerin and tumour necrosis factor receptor. The cDNA was
CC isolated from a heart cDNA library using mouse NTR-5 cDNA (see
CC X59345) as probe. Homology to osteoprotegerin suggests that NTR-5
CC is involved in the regulation of bone mass, and may be useful for
CC regulating development, proliferation and death of osteoblast or
CC osteoclast cells or for regulating muscle metabolism, and that it
CC may be implicated in muscle diseases or disorders. A host-vector
CC system for production of NTR-5 is claimed. NTR-5 polypeptides can
CC be used as immunogens and in screening assays to identify NTR-5
CC ligands, agonists and antagonists. The NTR-5 polynucleotide is
CC useful as a diagnostic tool, and as a source of probes and primers.
CC The invention also provides for diagnostic and therapeutic methods
CC based on the interaction of NTR-5 and agents that initiate signal
CC transduction through binding to NTR-5.
XX XX
SQ Sequence 987 BP; 220 A; 251 C; 278 G; 238 T; 0 other;

Query Match 55.9%; Score 835.6; DB 20; Length 987;
Best Local Similarity 99.5%; Pred. No. 4e-167;
Matches 838; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 45 atggtcttaaaagtctactagaacaagaaaaacgtttttcactcttttagtattacta 104
Db 1 atggtcttaaaagtctactagaacaagaaaaacgtttttcactcttttagtattacta 60
Qy 105 ggcattttgcatgtaaaagtactgtgaaacagagagactgtagacagagaattcagg 164
Db 61 ggcattttgcatgtaaaagtactgtgaaacagagagactgtagacagagaattcagg 120
Qy 165 gatcggctctgaaactgtttccctgcaaccagtggtggccagcatgagttgctaaag 224
Db 121 gatcggctctgaaactgtttccctgcaaccagtggtggccagcatgagttgctaaag 180
Qy 225 gaatgtgcttcggtatgggagagatgcacagtggtgacgtgcggtcgcacaggttc 284
Db 181 gaatgtgcttcggtatgggagagatgcacagtggtgacgtgcggtcgcacaggttc 240
Qy 285 aaggagagactgggcttcagaaaaatgcagccctgtctggactgcgagtggtgaaccgc 344
Db 241 aaggagagactgggcttcagaaaaatgcagccctgtctggactgcgagtggtgaaccgc 300
Qy 345 ttccagaagcaaatgttcagccaccagtgatgcatcctcgggagactgcttgcaggaa 404
Db 301 ttccagaagcaaatgttcagccaccagtgatgcatcctcgggagactgcttgcaggaa 360
Qy 405 ttctataggaagacgaaactgtcggtttcaagacatggagtggtgctcttgagagac 464
Db 361 ttctataggaagacgaaactgtcggtttcaagacatggagtggtgctcttgagagac 420
Qy 465 cctcctccttaccgaaccgcaactgtgtccagcagaggccaacctgtgaaagatcgctcc 524


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Db 649 gcaagaggcagttcattgagagaaccacccagctggtctctcgtggtcacagacattcagt 708
Qy 682 acaacgctctgagctgctgtcttgacacacctcagctcacgaatatccacaag 741
Db 709 acaatggctctgagctgctgcttgacacacccctcgcctcgcctcgtgccatagag 768
Qy 742 cctgctccagctcgcgcgtgactcagtgacagacccctggtggtggtggtggtcccat 801
Db 769 catgctgcagtataccggaactcagcccaatgatatggcctgttcacactgattcgt 828
Qy 802 ccatgtctgtagagagcctgcagcccccaccccgccgactcttgggtggtgggtgcatt 861
Db 829 cctgtgtgtagagagcccgagctctgcccagagctgctgtgctgtggtggtgcgt 888
Qy 862 ctgcagcagctctcagacaagaacacgagcccgagcgagagagatgctgcgacttct 921
Db 889 ctccactaccctcagagagaaccgcgtctctgtggtggaacacagatgccagcctct 948
Qy 922 tcggtaccctcagcagctccatctgtggtgaggttttcagatgctggtggtggtggtg 981
Db 949 ttggtctgtttcccgctccatctgcgcgaggtttctgagctggtggtggtggtggt 1008
Qy 982 atccatcgtggtggtgacacatctcttttctgagctcttctgacactctgacactgagagaag 1041
Db 1009 atcctctggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1065
Qy 1042 acattcattctcattcaatcagaactgaaagctcaactcatttgcattcaaatcagctc 1101
Db 1066 ataccaatctccatcccaacccgaaagacagcagctctggtggtggtggtggtggt 1125
Qy 1102 aagattggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1161
Db 1126 aggtatggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1185
Qy 1162 ctgatttctagatataacacacacacacacacacacacacacacacacacacacacac 1221
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Qy 1222 ctatgagaagcagctagatcagagagatggtggtggtggtggtggtggtggtggtg 1281
Db 1246 ggaactccaaagcagaggtggtggtggtggtggtggtggtggtggtggtggtggt 1305
Qy 1282 cctccagg 1290
Db 1306 cctccagg 1314

RESULT 8
ID X23414
XX X23414 standard; DNA: 886 BP.
AC X23414;
XX
DT 18-JUN-1999 (first entry)
XX
DE Mouse mAP04-alpha (short) DNA.
KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW developmental abnormality; gestational abnormality; prostate cancer;
KW APO6; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW apoptosis; mouse; mAP04-alpha; ss.
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 72..716
FT /*tag= a
FT /product= "mAP04-alpha short"
XX
PN WO9111791-A2.
XX 11-MAR-1999.
PD
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```
XX PF 04-SEP-1998; 98WO-US18393.
XX PR 05-SEP-1997; 97US-0924634.
XX PA (UNIW ) UNIV WASHINGTON.
XX PI Chaudhary PM;
XX WPI: 1999-205191/17.
XX P-PSDB: W93580.
XX
XX New Tumor Necrosis Factor family receptor polypeptides and ligands -
XX useful for diagnosis and treatment of prostate cancer and
XX developmental or gestational abnormalities
XX
XX Example IV; Fig 7B; 156pp; English.
XX
XX This invention describes isolated Tumor Necrosis Factor (TNF) family
XX receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
XX fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
XX their active fragments. APO4 is useful for diagnosing prostate cancer
XX by determining levels of APO4 in an individual. Prostate cancer can also
XX be treated using APO4 selective binding agents linked to a therapeutic
XX moiety. APO4 polypeptides are also useful for identifying selective
XX binding agents, useful in diagnosis/treatment of disease by binding of
XX agents to the polypeptide/active fragment which is extracellular, or
XX expressed on the cell surface. The binding is preferably performed in
XX vivo. APO4 polypeptides/ active fragments are also useful for screening
XX for agonists and antagonists by binding and observing the change in APO4
XX activity. Effective pharmacological agents useful in diagnosis or
XX treatment of disease are also identified using APO4 polypeptides/active
XX fragments and APO4 signal transducer molecules that specifically interact
XX with a cytoplasmic domain of APO4 and detecting a change in level of APO4
XX activity. The method is performed in vivo or in vitro. APO polypeptides
XX are all useful as immunogens for preparing antibodies. APO4 is also
XX useful for diagnosis/treatment of developmental or gestational
XX abnormalities. APO8 was transfected to human breast carcinoma cell line
XX MCF-7, and induced apoptosis.
XX
XX Sequence 886 BP; 204 A; 245 C; 247 G; 190 T; 0 other;
XX
XX Query Match 30.8%; Score 460.8; DB 20; Length 886;
XX Best Local Similarity 81.9%; Pred. No. 2.8e-88;
XX Matches 531; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
Qy 22 aataacatttgataagaagatggctttaaaagtgtactagaacagaagaacgt 81
Db 49 aataaacacgtttgtgagagccatggcactcaaggctcctactctacacaggacgtgc 108
Qy 82 ttttcactcttttagtattactagctatttgcattgataaagtgtgtgaaacaggag 141
Db 109 tcttcgtgcattctcttctactccactgcatgtaagtgtggtggtggtggtggtggt 168
Qy 142 actgtagacagcaagaattcagggtcgtgtggaactgtgttccctcgaacacgtgtg 201
Db 169 attgaggcagcaggaattccaaggatcgatctggaactgtgtcctctgcaaacagtg 228
Qy 202 gggcaggcagtgagttgttaagaagtgtggtctcggtctatgggaggtggtcacagtgtg 261
Db 229 gacctggcagtgagttgtccaaggatgtggtctcggtctatgggaggtggtcacagtgtg 288
Qy 262 tgacgtgcggctgcacaggttccaaggaggtggtggttccagaaaatgcgaacccctgtc 321
Db 289 tgccctgcagcgccagcgttccaaggaggtggttccagaaagtgttaagcctgtg 348
Qy 322 tggactgcgcagtggtgaaccgcttccagaagcgaattgttcagccacacagtgatgcc 381
Db 349 cggactgtgctgtggaaccgcttccagaagggcgaactgtctcacacacagtgatgctg 408
Qy 382 tctgcgggagctgcttgcagagattttataggaaagacgaaactgtcggtcttcaagaca 441
XX
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Db 409 tctgcgggggactcctgcaggattttaccggaagaccacaaactggtgttttcaagaca 468
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 Db 469 tggagtgctgctgcggagaccacacctctctctacgaaccacactgtaccagcaagg 528
 QY 502 tcaacctgtgaagatcgctccacgcctccagccacacgggacacggcgctgctgccc 561
 Db 529 tgaacctgtgaagatctctccacgcgtctccagcctccagcgcgtgctgccc 588
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 Db 589 tcatctgcagtgctgcccacgcgtgctgctgcccctgctcatctctgtgtcatctatt 648
 QY 622 gtaagagacagtgtatggagaagaacacacacagctggtctctgcggtcac 669
 Db 649 gcaagggcagttcatggagaagaacacacacagctgttaagctcccatccc 696

RESULT 9
 X24977
 ID X24977 standard; cDNA; 942 BP.
 XX
 AC X24977;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Mouse TRAIN-R (long form) cDNA.
 XX
 KW TRAIN-R; receptor; mouse; tumour necrosis factor receptor;
 KW agonist; antagonist; cancer; immunological disease; therapy;
 KW cytosstatic; ss.
 OS
 XX Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 101..745
 FT /*tag= a
 XX
 PN W09913078-A1.
 XX
 PD 18-MAR-1999.
 XX
 PF 11-SEP-1998; 98WO-0519030.
 XX
 PR 06-MAY-1998; 98US-0084422.
 PR 12-SEP-1997; 97US-0058631.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Hession C, Tschopp J;
 XX
 DR WPI; 1999-229238/19.
 DR P-PSDB; W98145.
 XX
 PT New cysteine-rich tumor necrosis factor receptor
 XX
 PS Claim 1; Page 26-27; 30pp; English.
 XX
 CC The present sequence encodes a novel murine cysteine-rich tumour
 CC necrosis factor receptor family member termed TRAIN-R (long form)
 CC (see W98145). Murine TRAIN-R is expressed at high levels in brain
 CC and lung, and at lower levels in liver, skeletal muscle and kidney.
 CC Cell death can be induced by administering an agent capable of
 CC inhibiting the binding of TRAIN-R to its ligand. A claimed method
 CC of treating, or reducing, the advancement, severity or effects of
 CC an immunological disease in a mammal comprises administering a
 CC pharmaceutical composition which comprises a TRAIN-R blocking agent,
 CC e.g. soluble TRAIN-R (see also W98144). TRAIN-R can be fused to an
 CC immunoglobulin molecule to produce a fusion protein which may be
 CC targeted to various sites. It can be used in binding assays, and
 CC to identify antagonists and agonists. Anti-TRAIN receptor
 CC antibodies can be used to reduce the severity of an immune response

CC or to treat cancer. TRAIN-R blocking agents can be used to reduce
 XX the severity or effects of an immunological disease (all claimed).
 SQ Sequence 942 BP; 219 A; 264 C; 258 G; 200 T; 1 other;
 Query Match 30.8%; Score 460.8; DB 20; Length 942;
 Best Local Similarity 81.9%; Pred. No. 2.8e-88;
 Matches 531; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
 QY 22 aataatacatattgataaagaatggtcttaaaagtctactacagaagaagaacgt 81
 Db 78 aataaacaacgtttgtgagagccatgacctcaaggtctactctacacagacggtgc 137
 QY 82 tttctacactctttagtattactactaggctattttgcatgtaaaagtgaactttggaacacggag 141
 Db 138 tctctgcgtccattctctctctctactccacctggcagtgaagtgagtgcgaacccggag 197
 QY 142 actgtagacagcaagaattcagggtgctgtgaaactgttccctgcaaccagtggtg 201
 Db 198 attgcaggcagcaggaattcaaggatcgatctggaactgtgctctgcaaacagtgcg 257
 QY 202 ggcaggcatggagttgtctaaaggaatgtggtctcggtatggtgggaggaagtcacagtggtg 261
 Db 258 gacctggcatggagttgtccaaaggaatgtggtctcggtatggtgggaggaagtcacagtggtg 317
 QY 262 tgacgtgcggctgcacaggttcaaggaggactggggttccagaaatgcaagccctgtc 321
 Db 318 tgccctgcaggccgcagccggttcaaggaggactggggttccagaaagtgtaagccatgtg 377
 QY 322 tggactgcgcagtggtgaaccgctttcagaaggcacaattgttccagccacagtgatgcc 381
 Db 378 cggactgcgcgtggtgaaccgctttcagaaggcacaactgtcacacacacagtgatgctg 437
 QY 382 tctgcggggactgctgcccaggattttataggaagacgaactgtcggtttcaagaca 441
 Db 438 tctgcggggactgctgcccaggattttaccggaagacacaaactggtgttttcaagaca 497
 QY 442 tggagtgctgctgtggagaccctctctctctctctctctacgaacgcactgtgccagaagg 501
 Db 498 tggagtgctgctgctgcggagaccacacctctctctctctctctctcaccacactgtaccagcaagg 557
 QY 502 tcaacctgtgaagatcgctccacgcctccagccacgggacacggcgctggtgcgcg 561
 Db 558 tgaacctgtgaagatctctctccacgcgtctccagccctcgggacacggcgctggtgcgcg 617
 QY 562 ttatctgcagcgtctgcccacgcgtctgctggtgcccctgctcatctctctgtgtcatctatt 621
 Db 618 tcatctgcagtgctgctgcccacgcgtgctgctgcccctgctcatctctgtgtcatctatt 677
 QY 622 gtaagagacagtgtatggagaagaacacacacagctggtctctgcggtcac 669
 Db 678 gcaagggcagttcatggagaagaacacacacagctgttaagctcccatccc 725

RESULT 10
 X87394
 ID X87394 standard; cDNA; 981 BP.
 XX
 AC X87394;
 XX
 DT 08-OCT-1999 (first entry)
 XX
 DE Mouse STRIPE1 (Tango 127a) cDNA.
 XX
 KW STRIPE1; Tango 127a; T127a; mouse; tumour necrosis factor receptor;
 KW sepsis; circulatory collapse; toxic shock; infection;
 KW immune disease; autoimmue disease; alcohol-induced hepatitis;
 KW inflammation; graft versus host pathology; cancer; tumour;
 KW cerebral malaria; multiple sclerosis; diagnosis; therapy; ss.
 XX
 OS Mus musculus.
 XX

FH Key Location/Qualifiers
 FT 1..106
 FT /*tag= a
 FT /note= "an isolated nucleic acid molecule
 FT comprising this region of the sequence is
 FT specifically claimed in Claim 3"
 FT CDS
 FT 107..751
 FT /*tag= b
 FT /product= STRIFE1
 FT /note= "an isolated nucleic acid molecule
 FT comprising the coding region is
 FT specifically claimed in Claim 2"
 FT sig_peptide
 FT 107..193
 FT /*tag= c
 FT 194..748
 FT /*tag= d
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 FT comprising the mature protein coding region
 FT is specifically claimed in Claim 14"
 FT 3'UTR
 FT 752..981
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 FT /note= "an isolated nucleic acid molecule
 FT comprising this region of the sequence is
 FT specifically claimed in Claim 4"
 FT WO9937818-A1.
 PN
 PD 29-JUL-1999.
 XX
 PF 27-JAN-1999; 99WO-US01679.
 XX
 PR 27-JAN-1998; 98US-0014195.
 XX
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 XX
 PI Busfield SJ;
 XX
 DR WPI; 1999-458707/38.
 DR P-PSDB; Y06522.
 XX
 PT New STRIFE1 and STRIFEII polypeptides, proteins and nucleic acid
 PT molecules useful for modulating TNFR associated disorders
 XX
 PS Claim 3; Fig 1A-B; 119pp; English.
 CC This is the nucleotide sequence of mouse STRIFE1 (also called
 CC Tango 127a or T127a) cDNA. It encodes a protein (see Y05422) that
 CC belongs to the tumour necrosis factor receptor (TNFR) superfamily.
 CC 2 Splice forms of murine STRIFE have been identified, one that is
 CC predicted to be membrane-bound (STRIFE1) and one that is secreted
 CC (STRIFE2, see Y06523). STRIFE was identified as a TNFR homologue
 CC by a computer-based search of public EST databases. The invention
 CC provides STRIFE1 and STRIFE2 polynucleotides and polypeptides, as
 CC well as fusion proteins, antigenic peptides and antibodies. It
 CC also provides expression vectors, host cells and transgenic
 CC animals, as well as diagnostic, screening and therapeutic methods.
 CC STRIFE I and STRIFE II may play a role in mediating inflammatory,
 CC immune and host defense functions and may play a role in various
 CC neoplastic disease states. They may be useful as targets for
 CC developing novel diagnostic and therapeutic agents for TNF- and
 CC TNFR-associated disorders. Examples include sepsis syndrome,
 CC circulatory collapse and shock resulting from bacterial infection,
 CC acute and chronic parasitic or infectious processes, acute and
 CC chronic immune and autoimmune pathologies, alcohol-induced
 CC hepatitis, chronic inflammatory pathologies, vascular inflammatory
 CC pathologies, graft-versus-host pathology, malignant pathologies
 CC involving TNF-secreting tumors, cerebral malaria and multiple
 CC sclerosis.
 XX
 SQ Sequence 981 BP; 247 A; 270 C; 264 G; 200 T; 0 other;

Query Match

30.8%; Score 460.8; DB 20; Length 981;

Best Local Similarity 81.9%; Pred. No. 2.9e-88;
 Matches 531; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
 Qy 22 aataaatacattgataaagaagatggctttaaaagtctactagaacaagaagaaacgt 81
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 84 aataaacacgtttgtgagagccatgacacaaaggtctcctctacacagagcgtgc 143
 Qy 82 ttctacactcttttagtattactagctattgtgcatgtaaaagtactgtgaaacagag 141
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 144 tcttgctgcatctctctctactccactggcatgtaaaagtactgtgaaacccgag 203
 Qy 142 actgtagacacaaagaattcaggagatcggtctgaaactgttccctgcacacagtg 201
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 204 attcgaggcagcaggaattcaagatcgatctggaactgtgctctctgcaaacagtcg 263
 Qy 202 ggcacggcatggagttgtctaaggaatgtgcttcggctatggggagagatgcacagt 261
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 264 gacctggcagagttgtccaaggaatgtgcttcggctatggggagagatgcacagt 323
 Qy 262 tgacgtgcccgtgcacaggttcaagggaggtcgggtctccagaaatgcgaagccctgtc 321
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 324 tgcctgcaggccgcacccggttcaaggaagactgggtttccagaagtgttaagccatgtg 383
 Qy 322 tggactgcagtggtgaaccgctttcagaaggcaaatgttccagccaccagtgatgcca 381
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 384 cggactgtgcgtgtgaaccgctttcagagggccaaactgtccacacaccagtgatgctg 443
 Qy 382 tctcggggagactgttgcaggattttataggaagacaaactgtcggctttcaagaca 441
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 444 tctcggggagactgctgcaggattttaccggaagacaaactgtgtgttttcaagaca 503
 Qy 442 tggagtgctgctgtgagacacctctctctcctacgaaccgacactgtgcccagaagg 501
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 Db 504 tggagtgctgctgtgagacacctctctctcctcctacgaaccacactgtaccagaagg 563
 Qy 502 tcaacctgtgaagatcgctccacggcctccagccacgggacacggcgctggctgcgg 561
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 Db 564 tgaaccttgtgaagatctctctccaccgtctccagccctcgggacacggcgtggctgcg 623
 Qy 562 ttatctcagcgctctgcccaccgtctcctgctgcccctcctcctcctcctcctcatt 621
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 Qy 622 gtaagacagactttatggagaagaacccagctgtgctcctcctcctcctcctcctc 669
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 684 gcaagaggcagttcatggagaagaacccagctgtgaagctccatccc 731
 RESULT 11
 X84622
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 XX
 AC X84622;
 XX
 DT 16-SEP-1999 (first entry)
 XX
 DE Human TNFR superfamily soluble receptor coding sequence.
 KW TNF1; human; TNFR superfamily; tumour necrosis factor ligand; TNF;
 KW tumour necrosis factor receptor; TNFR superfamily; cell proliferation;
 KW cell differentiation; cytokine production; immunoglobulin; hyperplasia;
 KW apoptosis inducer; activated T cell; autoimmune disease; inhibitor;
 KW myasthenia gravis; insulin-dependent diabetes mellitus; endotoxin shock;
 KW rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
 KW tumour; proliferative disorder; neoplasia; dysplasia; immunocompetence;
 KW lymphoid organogenesis; bacterial resistance; contact hypersensitivity;
 KW delayed type sensitivity; therapy; ss.
 OS Homo sapiens.
 XX
 PN WO9933980-A2.
 XX
 PD 08-JUL-1999.

XX 11-MAR-1999.
 PD 04-SEP-1998; 98WO-US18393.
 PF 05-SEP-1997; 97US-0924634.
 PR (UNIW) UNIV WASHINGTON.
 PA Chaudhary PM;
 PI WPI; 1999-205191/17.
 XX P-PSDB; W93583.
 DR New Tumor Necrosis Factor family receptor polypeptides and ligands -
 PT useful for diagnosis and treatment of prostate cancer and
 PT developmental or gestational abnormalities
 XX
 PS Disclosure; Fig 7E; 156pp; English.
 XX This invention describes isolated Tumor Necrosis Factor (TNF) family
 CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
 CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
 CC their active fragments. APO4 is useful for diagnosing prostate cancer
 CC by determining levels of APO4 in an individual. Prostate cancer can also
 CC be treated using APO4 selective binding agents linked to a therapeutic
 CC moiety. APO4 polypeptides are also useful for identifying selective
 CC binding agents, useful in diagnosis/treatment of disease by binding of
 CC agents to the polypeptide/active fragment which is extracellular, or
 CC expressed on the cell surface. The binding is preferably performed in
 CC vivo. APO4 polypeptides/ active fragments are also useful for screening
 CC for agonists and antagonists by binding and observing the change in APO4
 CC activity. Effective pharmacological agents useful in diagnosis or
 CC treatment of disease are also identified using APO4 polypeptides/active
 CC fragments and APO4 signal transducer molecules that specifically interact
 CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
 CC activity. The method is performed in vivo or in vitro. APO polypeptides
 CC are all useful as immunogens for preparing antibodies. APO4 is also
 CC useful for diagnosis/treatment of developmental or gestational
 CC abnormalities. APO8 was transfected to human breast carcinoma cell line
 CC MCF-7, and induced apoptosis.
 XX Sequence 591 BP; 148 A; 145 C; 175 G; 123 T; 0 other;

Query Match 21.8%; Score 326.6; DB 20; Length 591;
 Best Local Similarity 78.2%; Pred. No. 4.3e-60;
 Matches 392; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

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 QY 78 aggttttccacttttagtattactaggtctatttgcattgaagtgtgtgaaaca 137
 DB 128 gtgcttctgctgccattctctactccaccgtgcattgaagtgtgtgaaacc 187
 QY 138 ggagactgtagacagacaagaattcaggatcggtctggaactgttccctgcaaccag 197
 DB 188 ggagattcaggcagcaggaattcaggatcgatcgtggaactgtgtcctctgcaaccag 247
 QY 198 tgtggtccagcagcaggtgtgtcgaagaatgtggtctcggtctatgggagagatgcacag 257
 DB 248 tgcggactgtgcatgaggtgtgtccagggaatgtggtctcggtctatgggagagatgcacag 307
 QY 258 tgtgtgactgtgctgctgcacaggttcaaggaggtcgggttccagaaatgcagacc 317
 DB 308 tgtgtgcttgcaggccgaccggttcaaggaggtcgggttccagaaatgcagacc 367
 QY 318 tgtctgagctgcagctgtgacccgttccagaggaatgttccagaccagctgat 377
 DB 368 tgtggtgactgtgcgtgtgtaacgcgttccagaggtggtccacactgtctcacaccagtgat 427

QY 378 gccatctcggggactgttgcaggattttatagaagaacgaactgtcgcgtttcaa 437
 DB 428 gctgtctcggggactgttgcaggattttaccggaagaaacaaactgtgtgtttcaa 487
 QY 438 gacatggagtgtgtccttctgtggagaccctctctctctacgaaccgacactgtgcagc 497
 DB 488 gacatggagtgtgtcctcgtcgagaccacactctctctctacgaaccacactgtgagtga 547
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 XX X24976;
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 XX 05-JUL-1999 (first entry)
 XX Mouse TRAIN-R (short form) cDNA.
 XX
 KW TRAIN-R; receptor; mouse; tumour necrosis factor receptor;
 KW agonist; antagonist; cancer; immunological disease; therapy;
 KW cytostatic; ss.
 XX
 OS Mus musculus.
 FH Key Location/Qualifiers
 CDS 104..556
 /tag= a
 XX
 PN W09013078-A1.
 XX
 PD 18-MAR-1999.
 XX
 PF 11-SEP-1998; 98WO-US19030.
 PR 06-MAY-1998; 98US-0084422.
 PR 12-SEP-1997; 97US-0058631.
 XX
 XX (BIOJ) BIOGEN INC.
 XX
 PI Hession C, Tschopp J;
 XX
 DR WPI; 1999-229238/19.
 DR P-PSDB; W98144.
 XX
 PT New cysteine-rich tumor necrosis factor receptor
 XX
 PS Claim 1; Page 26; 30pp; English.
 XX
 CC The present sequence encodes a novel murine cysteine-rich tumour
 CC necrosis factor receptor family member termed TRAIN-R (short form)
 CC (see W98144). This putative natural soluble form of murine TRAIN-R
 CC may inhibit signalling by the full-length TRAIN-R (see W98145).
 CC Murine TRAIN-R is expressed at high levels in brain and lung, and
 CC at lower levels in liver, skeletal muscle and kidney. Cell death
 CC can be induced by administering an agent capable of inhibiting the
 CC binding of TRAIN-R to its ligand. A claimed method of treating, or
 CC reducing, the advancement, severity or effects of an immunological
 CC disease in a mammal comprises administering a pharmaceutical
 CC composition which comprises a TRAIN-R blocking agent, e.g. soluble
 CC TRAIN-R. TRAIN-R can be fused to an immunoglobulin molecule to
 CC produce a fusion protein which may be targeted to various sites.
 CC It can be used in binding assays, and to identify antagonists and
 CC agonists. Anti-TRAIN receptor antibodies can be used to reduce the
 CC severity of an immune response or to treat cancer. TRAIN-R
 CC blocking agents can be used to reduce the severity or effects of an
 CC immunological disease (all claimed).
 XX Sequence 599 BP; 149 A; 147 C; 180 G; 123 T; 0 other;

Query Match	21.8%;	Score 326.5;	DB 20;	Length 599;
Best Local Similarity	78.2%;	Prod. No. 4.3e-60;		
Matches 392;	Conservative	0;	Mismatches 109;	Indels 0; Gaps 0;
18	caacataaatacatttgataagaagaatgaccttaaaagtgctactagaacaagagaaa	77		
77	caggataaacacgcttggtgagagccatggcactcaagggtctctacctctacacaggacg	136		
78	acgtttttcactcttttagtattactagctatttgcctataaagtgactttgtaaacaa	137		
137	gtgctctcgctgccattctcttctactccacctggcatgtaaaagtgagttgcgaacc	196		
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197	ggagattgcaggcagcaggaattcaaggatcgatctggaacctgtctctctgcaaacg	256		
198	tgtgggcccagcgcatggagttgctcaaggaatggcttcggtctagggagatgcacag	257		
257	tgcggaccttgcatggagctgtcccaaggaaatggcttcggctcagggagatgcacag	316		
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378	gccacttcggggactgcttgcaggattttatagaagacgaaacttgtcgctttcaa	437		
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498	aagggtcaacctcgtggaagatc	518		
557	tgtgccaaagtggcagcagacc	577		

Search completed: March 3, 2001, 04:42:02
Job time: 18591 sec

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RESULT      5
US-08-747-221B-38/c
: Sequence 38, Application US/08747221B
: Patent No. 6063610
: GENERAL INFORMATION:
: APPLICANT: Silver, Gary W.
: APPLICANT: Wisniewski, Nancy
: TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
: TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
: NUMBER OF SEQUENCES: 66
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Carol Talkington Verser, Ph.D.
: ADDRESSEE: Heska Corporation
: STREET: 1825 Sharp Point Drive
: CITY: Fort Collins
: STATE: Colorado
: COUNTRY: USA
: ZIP: 80525
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: Windows 95
: SOFTWARE: Wordperfect for Windows, Version 7.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/747,221B
: FILING DATE: NO. 6063610ember 12, 1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Verser, Carol Talkington
: REGISTRATION NUMBER: 37,459
: REFERENCE/DOCKET NUMBER: FC-1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 970/493-7272

```

Query Match 3.5%; Score 52.8; DB 1; Length 5173;
Best Local Similarity 67.0%; Pred. No. 0.00086;

RESULT 10

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 991 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: SOYBEAN
; IMMEDIATE SOURCE:
; CLONE: SSM.PK0067.G5
; US-08-924-747-25

Query Match 3.4%; Score 51.2; DB 3; Length 991;
Best Local Similarity 64.2%; Pred. No. 0.001;
Matches 77; Conservative 0; Mismatches 43; Indels 0; Gaps

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Db 846 TGTCTGTTTTAAATTAATTGACTGTGTTGGTGGGTATTCGCTATTTTAAATTTTAA 905
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 906 CTAAAAAAGTGTTCAGTTTTTAAAAAATAAAAAAATAAAAAAATAAAAAAATA 965
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RESULT 13
US-08-655-352-10
; Sequence 10, Application US/08655352
; Patent No. 607791
; GENERAL INFORMATION:
; APPLICANT: Bachattira W. Poovaiah, zhihua Liu,
; APPLICANT: Shameekumar Patil, Daisuke Takezawa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh &
ADDRESS: Whinston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,352
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,449
FILING DATE: October 14, 1994
ATTORNEY/AGENT INFORMATION: *
NAME: Dow, Alan, E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-45000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 20:24:05 ; Search time 889.38 seconds
(without alignments)
11787.089 Million cell updates/sec

Title: US-09-380-276A-7
Perfect score: 1496
Sequence: 1 gggaaacgtagaactctccaa.....aaaaaaaaaaaaaaaaaaaa 1496

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues
Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	425.2	28.4	454	147	W56629	zdl6e11.r1
2	302.2	20.2	395	106	BE306459	BE306459 601103459
3	274.8	18.4	282	28	AL036000	AL036000 DKFp564K
4	264.8	17.7	534	135	BE757704	BE757704 212225 MA
5	215.6	14.4	401	1	AA003356	AA003356 mg4901.r
6	192.8	12.9	369	91	AA036247	AA036247 ml74a03.r
7	186.6	12.5	358	1	AA036247	AA036247 ml74a03.r
8	157.6	10.5	258	133	BB542020	BB542020 BB542020
9	155	10.4	643	159	AQ563354	AQ563354 HS_5335-B
10	125.8	8.4	646	159	AQ544065	AQ544065 RPCI-11-3
11	124.4	8.3	275	31	AV111112	AV111112 AV111112
12	120.8	8.1	404	8	AA495217	AA495217 fa04d10.r
13	113.8	7.6	450	158	AQ514075	AQ514075 HS_5184-A
14	95	6.4	1110	193	CNS0507C	AL347097 Tetraodon
15	91.2	6.1	414	91	AW527025	AW527025 UI-R-B01-
16	80.2	5.4	381	21	AI551729	AI551729 vflle02.y
17	67.4	4.5	442	109	BE554624	BE554624 ur48c11.y
18	63	4.2	996	138	BE966927	BE966927 601660947
19	62	4.1	240	29	AU074171	AU074171 AU074171
20	61.8	4.1	240	29	AU074171	AU074171 AU074171
21	61.6	4.1	734	191	CNS024WE	AL181319 Tetraodon
22	61.2	4.1	207	29	AU037991	AU037991 AU037991
23	61	4.1	495	10	AA676361	AA676361 ad38a04.s
24	61	4.1	746	191	CNS0330X	AL226410 Tetraodon
25	60.8	4.1	357	140	C91149	C91149 C91149 Dict
26	60.8	4.1	591	87	AW187044	AW187044 BNLC1918
27	60.4	4.0	710	106	BE317688	BE317688 NF053F10L
28	60.2	4.0	434	111	BE722937	BE722937 192212 MA
29	59.8	4.0	153	190	CNS0151E	AL105488 Drosophila
30	59.8	4.0	786	190	CNS009A5	AL053317 Drosophila
31	59.8	4.0	928	190	CNS00DKY	AL071865 Drosophila
32	59.6	4.0	583	192	CNS044QG	AL274417 Tetraodon
33	59.2	4.0	231	3	AA185470	AA185470 mu47f06.f
34	59.2	4.0	497	29	AU038067	AU038067 AU038067
35	59.2	4.0	625	191	CNS036A2	AL229763 Tetraodon
36	59.2	4.0	690	140	C93837	C93837 C93837 Dict
37	59.2	4.0	996	138	BE966927	BE966927 601660947
38	59.2	4.0	1101	190	CNS00238	AL097166 Drosophila
39	59	3.9	405	150	AQ173919	AQ173919 HS_3204-A
40	59	3.9	495	93	AW644074	AW644074 cm37b04.w
41	58.8	3.9	586	191	CNS02B9C	AL189561 Tetraodon
42	58.4	3.9	330	29	AU037574	AU037574 AU037574
43	58.4	3.9	362	23	AI673278	AI673278 tw69e12.x
44	58.4	3.9	637	191	CNS036CC	AL229845 Tetraodon
45	58.4	3.9	867	190	CNS00CX5	AL060052 Drosophila

ALIGNMENTS

RESULT 1

W56629
 LOCUS
 DEFINITION W56629 454 bp mRNA
 zdl6e11.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
 IMAGE:340844 5', mRNA sequence.
 ACCESSION W56629
 VERSION W56629.1 GI:1358487
 KEYWORDS EST.
 SOURCE human.

Db 181 GGTTCAGGAAGACTGGGTTTCCAGAACTGTAAGCGGTGTGCGGACTGTGCGCTGGTGA 240
 QY 340 accgcttcagaaagcaaaattgttcagccaccagtgatgccatctgcgggactgtctgc 399
 Db 241 ACCGCTTTAGAGGGCAACTGCTCACACCACTAGTATGCTGCGGGGACTGCGCTG 300
 QY 400 caggatttatagaagacgaactgtcggtttcaagacatggagtggtgctccttg 459
 Db 301 CAGGATTTACCGGAAGACCAAACTGGTTGTTTCAAGACATGGAGTGTGCGCCCTGG 360
 QY 460 gagacctctctctcttcaagaccgcaactgtgccc 494
 Db 361 GAGACCCACTCTCCCTACGAAACCACTGTACC 395

RESULT 3

AL036000 282 bp mRNA EST 29-FEB-2000
 LOCUS DKF2p564K1022.r1 564 (synonym: hfb2) Homo sapiens cDNA clone
 DEFINITION DKF2p564K1022 5', mRNA sequence.
 ACCESSION AL036000
 VERSION AL036000.1 GI:5405629
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 282)
 AUTHORS Wambutt,R., Heubner,D., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
 TITLE EST (Wambutt, et al.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Wambutt R
 MIPS

An Klopferspitz 18a D-82152 Martinsried, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
 consortium of the German Genome Project.
 sl sequence also available.

This clone (DKF2p564K1022) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

Location/Qualifiers
 1..282
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 /db_xref="taxon:9606"
 /clone="DKF2p564K1022"
 /clone_lib="564 (synonym: hfb2)"
 /tissue_type="brain"
 /dev_stage="fetal"
 /lab_host="xl-2blue"
 /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

BASE COUNT 57 a 85 c 75 g 63 t 2 others
 ORIGIN

Query Match 18.4%; Score 274.8; DB 28; Length 282;
 Best Local Similarity 98.6%; Pred. No. 9.8e-52;
 Matches 276; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 409 ataggagacgaactgttcggtttcaagacatggagtggtgcttggagaccctc 468
 Db 3 ATAGGAAGACGAACCTGTTCGGCTTTCAAGACATGAGTGTGCGCTGTGGAGACCCCTC 62
 QY 469 ctctctcttacgaaccgcaactgttcagcaaggtcaacctcgttgaagatcgctccacgg 528
 Db 63 CTCTCTCTTACGAACCGCACTGTGCCAGGTCAGCAAGGTCAACCTCGTGAAGATCGCGCTCCACGG 122
 QY 529 cctccagccacggagacggcctgctgctgttatctgacgcctctggccaccgtcc 588
 Db 123 CTCCAGCCCCACGGGACACGGCGCTGGCTGCGCTTATCTGCANCGCTCTGGCCACCGCTCC 182

QY 589 tgcgtgccctgcctcctctgtgtcatctattgttaagacacagtttatgagagaac 648
 Db 183 TGCTGCCCTGCTCATCCCTGTGTGTCATCTATTGTAAAGACAGTTTATGGAGAANAAC 242
 QY 649 ccagctggctctgcgtgcacagagcattcagtcacaacgg 688
 Db 243 CCAGCTGGTCTCTGCGGTGCGANGACATTCAGTACTACGG 282

RESULT 4

BE757704 534 bp mRNA EST 15-SEP-2000
 LOCUS 212225 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
 DEFINITION BE757704
 ACCESSION BE757704
 VERSION BE757704.1 GI:10171696
 KEYWORDS EST.
 SOURCE COW.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 534)
 AUTHORS Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
 Bennett,G.A., Fahrénkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid,
 W.W. and Keele,J.W.
 TITLE Design and use of four pooled tissue normalized cDNA libraries for
 EST discovery in cattle
 JOURNAL Unpublished (2000)
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACACAGCTATGACCAT

BACKWARD: GTTTCACGATCAGCAGC

Plate: 65 row: C column: 2

Seq primer: ATTTAGGTGACACTATAG.

FEATURES

Location/Qualifiers
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 /db_xref="taxon:9913"
 /clone_lib="MARC 2BOV"
 /tissue_type="pooled"
 /lab_host="DH108"
 /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
 Library made from pooled tissue from testis, thymus,
 semitendinosus muscle, longissimus muscle, pancreas,
 adrenal, and endometrium."

BASE COUNT 122 a 117 c 171 g 124 t
 ORIGIN

Query Match 17.7%; Score 264.8; DB 135; Length 534;
 Best Local Similarity 82.9%; Pred. No. 1.9e-49;
 Matches 315; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY 7 gtagaactctcccaataataacatttgataagaagatggctttaaagtgctactag 66
 Db 158 GAAGACTCTTCAACCCAGAAATACATTATAAGACCAATGGCTTCAACCTGCTACTCA 217
 QY 67 aacaagaaaaacgttttcaactcttttagtattactaggtatttgcataagtgta 126
 Db 218 GGCAACAGAAA---TCTTTACCGTGTGTAGTCTTTTACTAGCTGTGTGGCATGTGGAGTGA 274
 QY 127 ctgtgaacacagagactgtacacagaagaattcagggatcggtctggaacgtgttc 186
 Db 275 TTTGTGAAACAGGAGAGCTGTGGACAGCAGGAATTCAGGGACCAGTCAGGAAGCTGTGTTTC 334

QY	187	ccctgcaaccagtgtggccaggcatgagtgattgtctaaggaaatgtggcttgcctatggg	246
Db	335	TTGTCAAAGCAGTGTGGCCAGGCAATGAGTTGTCCAAGGAATGTGGCTTACGGGG	394
QY	247	agatgcacacagtgtgacatgcgcgtgcacaggttcaaggagactgggcttcaga	306
Db	395	AGGACGCCCAAGTGTGAAGTGGCCGCCGACAGGTTCAAGGAGACTGGGGCTCTCAGA	454
QY	307	aatgcaagccctgtctggaactgcgcagtgtgaaccgctttcagaagcaaatgttcag	366
Db	455	AGTGCAAGCCGTGCTGGACTGCGCCCTGCTGTGAGCGCTTCACAGAAGCCAACTGCTCGG	514
QY	367	ccaccagtgatgcatactgc	386
Db	515	CCACTGGCGACGGCGTCTGC	534
RESULT	5		
AA003356			
LOCUS			
DEFINITION	AA003356	401 bp mRNA	EST 19-JUL-1996
	mg4901.r1 Soares mouse embryo NBME13.5 14.5 Mus musculus cDNA		
ACCESSION	AA003356		
VERSION	AA003356.1	GI:1446796	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 401)		
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Stepcoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Willson,R. and Waterston,R.		
TITLE	The WashU-HMI Mouse EST Project		
JOURNAL	Unpublished (1996)		
COMMENT	Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:261704 Seq primer: ETPrimer High quality sequence stop: 345. Location/Qualifiers 1. .401 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="IMAGE:427152" /clone_lib="Soares mouse embryo NBME13.5 14.5" /sex="unknown" /tissue_type="embryo" /dev_stage="13.5-14.5dpc total fetus" /lab_host="DH10B" /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTACCAATCTGAAGTGGAGCGCGCGAAATTTTTTTTTTTTTTTTTTTTTT T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru KO, Wayne State Univ., from 2 l]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."		
FEATURES			
source			

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The Institute of Physical and Chemical Research (RIKEN), Genomic
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Fax: +81-298-36-9098
Email: genome-res@rtc.riken.go.jp,
URL: <http://genome.rtc.riken.go.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki,
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermotabilization and thermoactivation of thermostable enzymes by
trehalose and its application for the synthesis of full length
cDNA. *Proc. Natl. Acad. Sci. U.S.A.* 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. *Genome Res.* 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

```

FEATURES
source
Location/Qualifiers
1. .258
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="E130118C08"
/clone_lib="RIKEN full-length enriched, 0 day neonate
eyeball"
/tissue_type="eyeball"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGCGCGCGCACTCGAGTTTTTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by the
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGAGATCTCGAGTTAATAATTAATCCCGCCCCCCCC 3']. cDNA
was cleaved with BamHI and XhoI. Vector: a modified
pBluescript KS(-) after bulk excision from Lambda FLC I.".
55 a 77 c 66 g
BASE COUNT
ORIGIN

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	Query Match	10.5%	Score 157.6;	DB 133;	Length 258;
	Best Local Similarity	80.7%;	Pred. No. 2.3e-25;		
	Matches 184;	Conservative 0;	Mismatches 44;	Indels 0;	Gaps 0;
QY	265	cftgcggcgtctcacaggttcaagagagacitggggtcttcagaatacgaaaccctgtctgg	324		
Db	1	CCTGCACCCGCCCGGTTCTAGAAGACTGGGCTTTCCAGAAGTGTAAAGCATGTGCGG	60		
QY	325	actgcgcagtgtgtaaacgcgttttcagaaggcaaatgttcagccaccagtgatgccatct	384		
Db	61	ACTTTGCGCTGTTGAACCGCTTTTCAGAGGCCCAACTGCTCACACCACACTGATGCTTTT	120		
QY	385	gcggggactcgtcgccggatttataggaagacgaacctgtcgcgctttcaagacatgg	444		
Db	121	CGGGGGACTCCTGCCAGGATTTTACCGGAGAGACAACCTGGTGGTTTTTCAGACATGG	180		
QY	445	agtgtgtgccttgbgagaccctcctcctccttacgaacgcgcactgtg	492		
Db	181	AGTGTCCTCCTGGGGAGACCCACTCCTCCTACGAACCCACTGTG	228		

9	RESULT	ACCESSION	REFERENCE	TITLE	JOURNAL
	AQ563354	VERSION	AUTHORS		MEDLINE
	LOCUS	KEYWORDS			COMMENT
	DEFINITION	SOURCE	ORGANISM		

BASE COUNT	Query Match	489
ORIGIN	Best Local	315
	Matches	
	Qy	549
	Db	375
	Qy	609
	Db	435
	Qy	669
	Db	495

RESULT 10
AQ544065
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AQ544065 646 bp DNA GSS 19-MAY-1999
RPCI-11-315F10-TV RPCI-11 Homo sapiens genomic clone RPCI-11-315F10
, DNA sequence.
AQ544065
GSS
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 646)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
, J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
Unpublished (1997)
Other_GSSs: RPCI-11-315F10.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbest@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .646
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/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3 6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"

BASE COUNT 175 a 135 c 145 g 191 t
ORIGIN

Query Match 8.4%; Score 125.8; DB 159; Length 646;
Best Local Similarity 94.9%; Pred. No. 3.7e-18;
Matches 130; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 655 ggtctctgcgggtcacagacattcagtcacacggctctgagctgtcgtgtcgttgacagac 714
|||||
Db 263 GGTCTGCGGGTCACAGGACATTCAGTACACGGCTCTGAGCTGCTGTTTGACAGAC 322
|||||
QY 715 ctcaagctcccaaatatgcccacagagcctcgtgccagtgcccgccgtgactcagtgacga 774
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Db 323 CTCAGCTCCACGAATATGCCACAGAGCCCTGCTGCCAGTCCCGCCGTGACTCAGTCAGA 382
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QY 775 cctgcgggcccgggtgcgc 791
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Db 383 CCTGCGGTAAAGTTCAGC 399
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RESULT 11
AV111112
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AV111112 275 bp mRNA EST 29-JUN-1999
AV111112 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA
clone 2600016N17, mRNA sequence.
AV111112

VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
BASE COUNT
ORIGIN

AV111112.1 GI:5265192
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 275)
Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara
, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,
Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H., Owa, C.,
Sato, K., Shibata, Y., Shigenoto, Y., Shiraki, T., Sogabe, Y., Sugahara
, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tomimaga, N.,
Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,
Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
RIKEN Mouse ESTs
Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
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77 a 86 c 55 g 57 t

Query Match 8.3%; Score 124.4; DB 31; Length 275;
Best Local Similarity 71.3%; Pred. No. 7e-18;
Matches 164; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 289 aggactggggcttccagaaatgcaagccctgtctgagctgcgcagtggtgaaccgcttc 348
|||||
Db 43 AAGAAAGTGGTTTCCAGAAAGTAAAGCCATTCGCCGAACCTGCGCTGTAGAACCCCTATC 102
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QY 349 agaagggcaattgttcagocccagctgagccatctgcgggggactgcttgcaggatttt 408
|||||
Db 103 TGAGGACCCATTCTCACACACACCTGATGCTCTCGCGGGACTGCTTGCCTGCAAGATTTT 162
|||||
QY 409 ataggagacgaactgttcggtcttcagacatgagtgagtgcttgcagagacccctc 468
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Db 163 ACCAGAGACCAAACTGGTTGGTTTTCAGACATGGAGTGTGTGCTCGGGAGACCCAC 222
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QY 469 ctctctctacgaacgcagcagctgtgcagcaaggtcgaacccgtggaagatc 518
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Db 223 CTCCTCCCTACGAACACACACAGTGAGTGATGTGCCAAGTGGCAGCAGACC 272
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RESULT 12
AA495217
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
BASE COUNT
ORIGIN

AA495217 404 bp mRNA EST 27-JUN-1997
fa04d10.r1 zebrafish ICRFzfls Danio rerio cDNA clone 10E17 5', mRNA
sequence.
AA495217
AA495217
AA495217.1 GI:2225645
EST.

[illegible]

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Db 207 TATTG 203

RESULT 14
LOCUS CNS050TC
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ACCESSION AL347097.1
VERSION 1110 bp DNA GSS 26-MAY-2000
KEYWORDS Tetraodon nigroviridis genome survey sequence T3 end of clone 042M15 of library C from Tetraodon nigroviridis, genomic survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Eurypterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha; Holacanthopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.
REFERENCE 1 (bases 1 to 1110)
AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,P., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1110)
AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,P., Saurin,W. and Weissenbach,J.
TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1110)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBSJ databases
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetraodon.
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ORIGIN

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Matches 139; Conservative 0; Mismatches 57; Indels 1; Gaps 1;

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Db 706 AGAATGTGGCTTTGGCTACGAGAGAGTGGCCGGTGTGTGCCCTGTGCGAGCGCCGCT 765
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|||||
QY 343 gtttcgaaggaatatttccagccaccagtagtgcacatct-ggggggactgcttgcca 401
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Db 826 GCTTCAGAGGCAACTGCTCCACGAGCAACGACGNTGGTGGAGACTGCCTGCC 885
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QY 402 ggaattttatagaagac 418
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Db 886 GGTCTAGTCAGCAGGCC 902
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RESULT 15
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DEFINITION UI-R-B01-ajg-f-10-0-UI.s1 UI-R-B01 Rattus norvegicus cDNA clone AW527025
ACCESSION AW527025
VERSION 414 bp mRNA EST 06-MAR-2000
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 414)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized mid-brain library cDNA Library Preparation: M.B. Soares
Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.
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        /strain="Sprague-Dawley"
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        /clone_lib="UI-R-B01"
        /dev_stage="adult"
        /lab_host="DH10B (Life Technologies)"
        /note="Vector: pT730-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The library (UI-R-B01) is a subtracted library derived from a mixture of the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at ratseq.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
        TAG_LIB=UI-R-B01
        TAG_ISSUE=mid-brain
        TAG_SEQ=GATGG"
BASE COUNT 91 a 102 c 94 g 127 t
ORIGIN

Query Match 6.1%; Score 91.2; DB 91; Length 414;
Best Local Similarity 58.5%; Pred. No. 2.2e-10;
Matches 159; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 1019 ttatcctgaactcactggagaagacattctctcaatccagacttgaagctcaac 1078
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Db 414 TTATCTGAACTCACCTGGAGAGATATCAATCTCCCTCAATCCCGAATCAAGCTCAAC 355
|||||
QY 1079 gtctttgattcaaatagcagtcagatttgggtggggtgttccagtcagtcactca 1138
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Db 354 ATCTGTGGATTCCAATGGTGTCTAGGATCTGGCTGGGCGAGTGTCTCCAGATTCTTCTGG 295
Qy 1139 ttctgaaaactttacagcagctactgatttattctagatataaacacacactggtagaatc 1198
Db 294 AGATTTTTCAGAAAATACTGACTCACCTAGATATGGTGACCCCGATAGCGGTCTGGGAGCA 235
Qy 1199 agcatcaactcagatgcactaaactatgagaagccagcctagatcaggagagtggcgctat 1258
Db 234 AACCCTAGCTCAGGATGCTCAAGGACTCCCAAGCAGAGAGGGCTGGGAAGCCAGTGAAAA 175
Qy 1259 catccaccagccactcagacgtccctccagg 1290
Db 174 CCTGAATCTAGCCACGTCACAGGCTTCCAGG 143

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